REMARKS

Applicants thank the Examiner for allowing claims 30-35, 41-45 and 51-63. Claim 17 has been cancelled without prejudice or disclaimer. Applicants reserve the right to pursue the canceled subject matter in a continuing application. Claims 30 and 32 have been amended to correct a minor, obvious error in claim order, placing claims 31 and 32 in proper dependent form and ensuring the further limitation of the subject matter of dependent claims 31 and 32, as required by 37 CFR 1.75(c). Claims 56 and 58 have likewise been amended to ensure the further limitation of the subject matter in dependent claims 57 and 58. None of these claim amendments are substantive, and therefore do not require any further search and consideration by the Examiner. As suggested by the Examiner, claims 64-66 have been amended to recite "the isolated polypeptide of claim 62" and claims 19 and 20 have been amended to depend from claim 56. No new matter has been added.

Upon entry of the present amendment, claims 19, 20, 30-35, 41-45 and 51-71 will be pending.

I. Election/Restrictions

Applicants thank the Examiner for deeming claim 19 available for rejoinder upon its amendment to establish proper dependency from an allowable claim. *See* lines 4-6 on page 4 of Paper No. 01292004. Pursuant to 37 CFR §1.116, claim 19 has been amended to comply with a requirement of form set forth in Paper No. 01292004. Specifically, claim 19 has been amended to depend from claim 56. In view of this amendment, Applicants respectfully request that claim 19 be rejoined with the allowed claims of elected group II.

II. Claim Objections

In the first paragraph on page 5 of Paper No. 01292004, claim 20 is objected to for depending from a claim drawn to a nonelected invention. Applicants submit that claim 20 has been amended to depend from allowable claim 56. As such, Applicants respectfully request that this objection be reconsidered and withdrawn.

III. Rejections under 35 USC §112, second paragraph

On page 5 of Paper No. 01292004, claims 64-66 are rejected for allegedly being indefinite. The Examiner further states that amending the claims to recite "the polypeptide of claim 62" would overcome this rejection.

Applicants submit that claims 64-66 have been amended to recite "the isolated polypeptide of claim 62." As such, Applicants request that this rejection be reconsidered and withdrawn.

IV. Double Patenting (Duplicate Claims) objection

On page 6 of Paper No. 01292004, claims 67-71 are objected to under 37 CFR 1.75 as allegedly being substantial duplicates of claims 51-55.

Applicants respectfully disagree and traverse.

Preliminarily, Applicants submit that this objection is not related to the doctrine of double patenting, which seeks to prevent the unjustified extension of patent exclusivity beyond the term of a patent, since the claims of only *one* patent are disputed. The issue of double patenting properly involves at least one issued patent and a pending patent application. *See* MPEP section 804. This is not the case here.

Regarding the issue of duplicative claims, Applicants assert that claims 67-71 are not substantial duplicates of claims 51-55 since the scope of these claims may be different. Section 706.03(k) of the MPEP states:

> Inasmuch as a patent is supposed to be limited to only one invention or, at most, several closely related indivisible inventions, limiting an application to a single claim, or a single claim to each of the related inventions might appear to be logical as well as convenient. However, court decisions have confirmed applicant's right to restate (i.e., by plural claiming) the invention in a reasonable number of ways. Indeed, a mere difference in scope between claims has been held to be enough.

Therefore, Applicants are entitled to restate (*i.e.,* by plural claiming) an invention in a reasonable number of ways.

Applicants submit that claims to a fragment of the polypeptide encoded by the HHEPU32 cDNA contained in ATCC Deposit No. 209603 and claims to a fragment of SEQ ID NO:108 are not necessarily identical in scope. As stated in the specification,

> ... DNA sequences generated by sequencing reactions can contain sequencing errors. The errors exist as misidentified nucleotides, or as

> insertions or deletions of nucleotides in the generated DNA sequence. The erroneously inserted or deleted nucleotides cause frame shifts in the reading frames of the predicted amino acid sequence. In these cases, the predicted amino acid sequence diverges from the actual amino acid sequence, even though the generated DNA sequence may be greater than 99.9% identical to the actual DNA sequence (for example, one base insertion or deletion in an open reading frame of over 1000 bases).
>
> Accordingly, for those applications requiring precision in the nucleotide sequence or the amino acid sequence, the present invention provides not only the generated nucleotide sequence identified as SEQ ID NO:X and the predicted translated amino acid sequence identified as SEQ ID NO:Y, but also a sample of plasmid DNA containing a human cDNA of the invention deposited with the ATCC, as set forth in Table 1. The nucleotide sequence of each deposited clone can readily be determined by sequencing the deposited clone in accordance with known methods. The predicted amino acid sequence can then be verified from such deposits. Moreover, the amino acid sequence of the protein encoded by a particular clone can also be directly determined by peptide sequencing or by expressing the protein in a suitable host cell containing the deposited human cDNA, collecting the protein, and determining its sequence.

See lines 7-26 on page 97 of the specification. Furthermore, the instant specification also teaches that the secreted polypeptide of SEQ ID NO: 108 may have alternate cleavage points, thus the secreted portion of the polypeptide encoded by the HHEPU32 cDNA in the ATCC Deposit may differ from that taught for SEQ ID NO: 108. *See* lines 4-25 of page 99 and the last row of Table 1 on page 94 of the specification. Thus, while the polypeptide of SEQ ID NO:108 is predicted to have a leader sequence of 18 amino acids, the polypeptide encoded by the HHEPU32 cDNA clone(s) deposited as ATCC Deposit No. 209603 may inherently have an alternative leader sequence. Applicants point out that previous statements made in Applicants' response dated November 6, 2003 acknowledge that the amino acid sequence of SEQ ID NO:108 *corresponds to* clone HHEPU32, which *relies on* the cDNA sequence contained in ATCC Deposit No. 290603. However, Applicants have not asserted that the amino acid sequence encoded by said deposit and that of SEQ ID NO:108 are 100% identical. Applicants further note that it is routine and widely accepted in biotechnology patent practice to claim isolated proteins by an explicit recitation of the amino acid sequences as well as those isolated from a corresponding deposited clone.

In view of the above remarks, Applicants respectfully submit that claims 67-71 are not substantial duplicates of claims 51-55 and, thus, should not be objected to under CFR 1.75. Applicants therefore respectfully request that this objection be reconsidered and withdrawn.

Conclusion

The Examiner is invited to call the undersigned at the phone number provided below if any further action by Applicant would expedite the examination of this application. If there are any fees due in connection with the filing of this paper, please charge the fees to our Deposit Account No. 08-3425.

Dated: March 26, 2004

Respectfully submitted,

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